

# SEQUENCE LISTING

<110> Reed, John C.  
Zapata, Juan M.

<120> Novel TRAF Family Proteins

<130> P-LJ 4453

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<150> US 09/434,784

<151> 1999-11-05

<160> 32

<170> PatentIn Ver. 2.0

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Met Asn His Gln Gln Gln Gln Gln Gln Lys

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Ala Gly Glu Gln Gln Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala

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Gly Asp Thr Asp Asp Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn

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 Glu Asp Asp Thr Ser Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val  
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 Lys Val Thr Phe Glu Val Phe Val Gln Ala Asp Ala Pro His Gly Val  
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 205 210 215

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 Gly Ala Thr Cys Tyr Met Asn Ser Leu Leu Gln Thr Leu Phe Phe Thr  
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Ser Asp Asn Glu Asn Pro Trp Thr Ile Phe Leu Glu Thr Val Asp Pro	
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Asp Val Met Leu Phe Leu Lys Met Tyr Asp Pro Lys Thr Arg Ser Leu	
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750 755 760	
gac atc ata gta ttt cag aag gat gac cct gaa aat gat aac agt gaa	2536
Asp Ile Ile Val Phe Gln Lys Asp Asp Pro Glu Asn Asp Asn Ser Glu	
765 770 775	
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Leu Pro Thr Ala Lys Glu Tyr Phe Arg Asp Leu Tyr His Arg Val Asp	
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Val Ile Phe Cys Asp Lys Thr Ile Pro Asn Asp Pro Gly Phe Val Val	
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 Asn Glu Asp Glu Tyr Glu Val Asn Leu Lys Asp Phe Glu Pro Gln Pro  
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 Gly Asn Met Ser His Pro Arg Pro Trp Leu Gly Leu Asp His Phe Asn  
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aaa gcc cca aag agg agt cgc tac act tac ctt gaa aag gcc att aaa 3496  
 Lys Ala Pro Lys Arg Ser Arg Tyr Thr Tyr Leu Glu Lys Ala Ile Lys  
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Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn Gly Asn Val Ala Leu  
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Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser  
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Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg  
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Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro  
85 90 95

Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln  
100 105 110

Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr  
115 120 125

Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg  
130 135 140

Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His  
145 150 155 160

Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val  
165 170 175

Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu  
180 185 190

Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys  
195 200 205

Lys His Thr Gly Tyr Val Gly Leu Lys Asn Gln Gly Ala Thr Cys Tyr  
210 215 220

Met Asn Ser Leu Leu Gln Thr Leu Phe Phe Thr Asn Gln Leu Arg Lys  
225 230 235 240

Ala Val Tyr Met Met Pro Thr Glu Gly Asp Asp Ser Ser Lys Ser Val



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Pro Val Gly Thr Lys Lys Leu Thr Lys Ser Phe Gly Trp Glu Thr Leu		
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Asp Asn Val Glu Asn Lys Met Lys Gly Thr Cys Val Glu Gly Thr Ile		
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Pro Lys Leu Phe Arg Gly Lys Met Val Ser Tyr Ile Gln Cys Lys Glu		
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Val Asp Tyr Arg Ser Asp Arg Arg Glu Asp Tyr Tyr Asp Ile Gln Leu		
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Ala Val Glu Gln Leu Asp Gly Asp Asn Lys Tyr Asp Ala Gly Glu His		
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Gly Leu Gln Glu Ala Glu Lys Gly Val Lys Phe Leu Thr Leu Pro Pro		
385	390	395 400
Val Leu His Leu Gln Leu Met Arg Phe Met Tyr Asp Pro Gln Thr Asp		
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Gln Asn Ile Lys Ile Asn Asp Arg Phe Glu Phe Pro Glu Gln Leu Pro		
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Leu Asp Glu Phe Leu Gln Lys Thr Asp Pro Lys Asp Pro Ala Asn Tyr		
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Tyr Val Val Tyr Leu Asn Pro Lys Gly Asp Gly Lys Trp Cys Lys Phe		
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Asn Tyr Gly Gly His Asp Asp Asp Leu Ser Val Arg His Cys Thr Asn		

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Glu Ala Asp Gly Asn Lys Thr Met Ile Glu Leu Ser Asp Asn Glu Asn		
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Pro Trp Thr Ile Phe Leu Glu Thr Val Asp Pro Glu Leu Ala Ala Ser		
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Gly Ala Thr Leu Pro Lys Phe Asp Lys Asp His Asp Val Met Leu Phe		
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Leu Lys Met Tyr Asp Pro Lys Thr Arg Ser Leu Asn Tyr Cys Gly His		
690	695	700
Ile Tyr Thr Pro Ile Ser Cys Lys Ile Arg Asp Leu Leu Pro Val Met		
705	710	715
Cys Asp Arg Ala Gly Phe Ile Gln Asp Thr Ser Leu Ile Leu Tyr Glu		
725	730	735
Glu Val Lys Pro Asn Leu Thr Glu Arg Ile Gln Asp Tyr Asp Val Ser		
740	745	750
Leu Asp Lys Ala Leu Asp Glu Leu Met Asp Gly Asp Ile Ile Val Phe		



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 Met Ser Arg Val Pro Ser  
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cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223  
 Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp  
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tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271  
 Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile  
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aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319  
 Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser  
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Ser	Thr	Phe	Ser	Ser	Gly	Ala	Asn	Asp	Lys	Leu	Lys	Trp	Cys	Leu	Arg	
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Val	Asn	Pro	Lys	Gly	Leu	Asp	Glu	Glu	Ser	Lys	Asp	Tyr	Leu	Ser	Leu	
				75					80					85		
tac	ctg	tta	ctg	gtc	agc	tgt	cca	aag	agt	gaa	gtt	cgg	gca	aaa	ttc	463
Tyr	Leu	Leu	Leu	Val	Ser	Cys	Pro	Lys	Ser	Glu	Val	Arg	Ala	Lys	Phe	
				90					95					100		
aaa	ttc	tcc	atc	ctg	aat	gcc	aag	gga	gaa	gaa	acc	aaa	gct	atg	gag	511
Lys	Phe	Ser	Ile	Leu	Asn	Ala	Lys	Gly	Glu	Glu	Thr	Lys	Ala	Met	Glu	
		105					110						115			
agt	caa	cgg	gca	tat	agg	ttt	gtg	caa	ggc	aaa	gac	tgg	gga	ttc	aag	559
Ser	Gln	Arg	Ala	Tyr	Arg	Phe	Val	Gln	Gly	Lys	Asp	Trp	Gly	Phe	Lys	
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Lys	Phe	Ile	Arg	Arg	Asp	Phe	Leu	Leu	Asp	Glu	Ala	Asn	Gly	Leu	Leu	
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cct	gat	gac	aag	ctt	acc	ctc	ttc	tgc	gag	gtg	agt	gtt	gtg	caa	gat	655
Pro	Asp	Asp	Lys	Leu	Thr	Leu	Phe	Cys	Glu	Val	Ser	Val	Val	Gln	Asp	
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Ser	Val	Asn	Ile	Ser	Gly	Gln	Asn	Thr	Met	Asn	Met	Val	Lys	Val	Pro	
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Glu	Cys	Arg	Leu	Ala	Asp	Glu	Leu	Gly	Gly	Leu	Trp	Glu	Asn	Ser	Arg	
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Phe	Thr	Asp	Cys	Cys	Leu	Cys	Val	Ala	Gly	Gln	Glu	Phe	Gln	Ala	His	
		200					205							210		
aag	gct	atc	tta	gca	gct	cgt	tct	ccg	gtt	ttt	agt	gcc	atg	ttt	gaa	847
Lys	Ala	Ile	Leu	Ala	Ala	Arg	Ser	Pro	Val	Phe	Ser	Ala	Met	Phe	Glu	
215					220					225				230		
cat	gaa	atg	gag	gag	agc	aaa	aag	aat	cga	gtt	gaa	atc	aat	gat	gtg	895
His	Glu	Met	Glu	Glu	Ser	Lys	Lys	Asn	Arg	Val	Glu	Ile	Asn	Asp	Val	
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 Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys  
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gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac 991  
 Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Asp  
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 Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys  
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 Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp  
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ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac 1135  
 Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn  
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tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg 1183  
 Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val  
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 Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser  
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agg 1642

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35 40 45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys  
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Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser  
65 70 75 80

Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Val Ser Cys Pro Lys Ser  
85 90 95

Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu  
100 105 110

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly  
115 120 125

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp  
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Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu  
145 150 155 160

Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met  
165 170 175

Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly  
180 185 190

Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly  
195 200 205

Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val  
210 215 220

Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg

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Phe	Ile	Tyr	Thr	Gly	Lys	Ala	Pro	Asn	Leu	Asp	Lys	Met	Ala	Asp	Asp
		260					265					270			
Leu	Leu	Ala	Ala	Ala	Asp	Lys	Tyr	Ala	Leu	Glu	Arg	Leu	Lys	Val	Met
		275				280					285				
Cys	Glu	Asp	Ala	Leu	Cys	Ser	Asn	Leu	Ser	Val	Glu	Asn	Ala	Ala	Glu
		290				295					300				
Ile	Leu	Ile	Leu	Ala	Asp	Leu	His	Ser	Ala	Asp	Gln	Leu	Lys	Thr	Gln
305					310					315					320
Ala	Val	Asp	Phe	Ile	Asn	Tyr	His	Ala	Ser	Asp	Val	Leu	Glu	Thr	Ser
			325					330					335		
Gly	Trp	Lys	Ser	Met	Val	Val	Ser	His	Pro	His	Leu	Val	Ala	Glu	Ala
		340						345				350			
Tyr	Arg	Ser	Leu	Ala	Ser	Ala	Gln	Cys	Pro	Phe	Leu	Gly	Pro	Pro	Arg
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Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val Phe Arg Cys Phe Ile	
20 25 30	



tgt atg gag aaa ttg cgg gat gca cgc ctg tgt cct cat tgc tcc aaa	144
Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser Lys	
35 40 45	
ctg tgt tgt ttc agc tgt att agg cgc tgg ctg aca gag cag aga gct	192
Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu Thr Glu Gln Arg Ala	
50 55 60	
caa tgt cct cat tgc cgt gct cca ctc cag cta cga gaa cta gta aat	240
Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val Asn	
65 70 75 80	
tgt cgt tgg gca gaa gaa gta aca caa cag ctt gat act ctt caa ctc	288
Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln Leu	
85 90 95	
tgc agt ctc acc aaa cat gaa gaa aat gaa aag gac aaa tgt gaa aat	336
Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu Asn	
100 105 110	
cac cat gaa aaa ctt agt gta ttt tgc tgg act tgt aag aag tgt atc	384
His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys Ile	
115 120 125	
tgc cat cag tgt gca ctt tgg gga gga atg cat ggc gga cat acc ttt	432
Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr Phe	
130 135 140	
aaa cct ttg gca gaa att tat gag caa cac gtc act aaa gtg aat gaa	480
Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn Glu	
145 150 155 160	
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Glu Val Ala Lys Leu Arg Arg Arg Leu Met Glu Leu Ile Ser Leu Val	
165 170 175	
caa gaa gtg gaa agg aat gta gaa gct gta aga aat gca aaa gat gag	576
Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg Asn Ala Lys Asp Glu	
180 185 190	
cgt gtt cgg gaa att agg aat gca gtg gag atg atg att gca cgg tta	624
Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met Met Ile Ala Arg Leu	
195 200 205	
gac aca cag ctg aag aat aag ctt ata aca ctg atg ggt cag aag aca	672
Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys Thr	
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Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser Leu Leu Gln Glu Val	
225 230 235 240	
 gag cac cag ttg cgg tct tgt agt aag agt gag ttg ata tct aag agc	768
Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys Ser	
245 250 255	
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Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met Ala	
260 265 270	
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Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu Val	
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Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr Leu	
290 295 300	
 cgt cag aga gca gat cct gtt tac agt cca cct ctt caa gtt tca gga	960
Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser Gly	
305 310 315 320	
 ctt tgc tgg agg tta aaa gtt tac cca gat gga aat gga gtt gtg cga	1008
Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val Arg	
325 330 335	
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Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro Glu	
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Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys Asn	
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Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp Phe Glu Val	
370 375 380	
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Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu Ala	
385 390 395 400	
 aat gaa gga tac ttg aat cca caa aat gat aca gtg att tta agg ttt	1248
Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg Phe	
405 410 415	

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Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His Trp	
420 425 430	
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Tyr Ile Thr Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln Ile	
435 440 445	
aac aac ctt aaa gag aga ctt act att gag ctg tct cga act cag aag	1392
Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln Lys	
450 455 460	
tca aga gat ttg tca cca cca gat aac cat ctt agc ccc caa aat gat	1440
Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn Asp	
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Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met Leu	
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ctc gaa ggt ggt cct act aca gct tct gta aga gag gcc aaa gag gat	1536
Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu Asp	
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Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu Leu	
515 520 525	
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Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val Asn	
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Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser Asn	
545 550 555 560	
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Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn Asp	
565 570 575	
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Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu Asp	
580 585 590	
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Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly Ser	
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Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr Ser	
610 615 620	
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Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp Leu	
625 630 635 640	
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Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg Pro	
645 650 655	
cct gct tca ctt ctg cag ccc aca gca tca tat tct cga aaa gat aaa	2016
Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp Lys	
660 665 670	
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Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu Lys	
675 680 685	
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Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met Lys	
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Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala Ala	
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Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala Leu	
725 730 735	
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Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly Met	
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Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn Ser	
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Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val Ala	
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 Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser Ser  
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 Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly Ser  
 820 825 830

atc ggt gat att ctg cca aaa act gaa gac cgg cag tgt aaa gct ttg 2544  
 Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala Leu  
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cat ctg gaa gga ctg cag atg act gat ttg gaa aat aat tct gaa act 2688  
 His Leu Glu Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu Thr  
 885 890 895

gga gag tta cag cct gta cta cct gaa gga gct tca gct gcc cct gaa 2736  
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gaa gga atg agt agc gac agt gac att gaa tgt gac act gag aat gag 2784  
 Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys Asp Thr Glu Asn Glu  
 915 920 925

gag cag gaa gag cat acc agt gtg ggc ggg ttt cac gac tcc ttc atg 2832  
 Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe Met  
 930 935 940

gtc atg aca cag ccc ccg gat gaa gat aca cat tcc agt ttt cct gat 2880  
 Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Phe Pro Asp  
 945 950 955 960

ggt gaa caa ata ggc cct gaa gat ctc agc ttc aat aca gat gaa aat 2928  
 Gly Glu Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu Asn  
 965 970 975

agt gga agg taattgccaa atcaagagaa ctgacttgca agctaccttg 2977  
 Ser Gly Arg

accctgaatt ttgctgtagt tgggtgctcaa atttgctatc agtcagataa tcagatttgg 3037

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10

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20

25

30

Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser Lys  
35 40 45

Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu Thr Glu Gln Arg Ala  
50 55 60

Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val Asn  
65 70 75 80

Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln Leu  
85 90 95

Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu Asn  
100 105 110

His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys Ile  
115 120 125

Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr Phe  
130 135 140

Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn Glu  
145 150 155 160

Glu Val Ala Lys Leu Arg Arg Arg Leu Met Glu Leu Ile Ser Leu Val  
165 170 175

Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg Asn Ala Lys Asp Glu  
180 185 190

Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met Met Ile Ala Arg Leu  
195 200 205

Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys Thr  
210 215 220

Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser Leu Leu Gln Glu Val  
225 230 235 240

Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys Ser  
245 250 255

Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met Ala  
260 265 270

Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu Val

275                      280                      285  
 Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr Leu  
 290                      295                      300  
 Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser Gly  
 305                      310                      315                      320  
 Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val Arg  
 325                      330                      335  
 Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro Glu  
 340                      345                      350  
 Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys Asn  
 355                      360                      365  
 Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp Phe Glu Val  
 370                      375                      380  
 Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu Ala  
 385                      390                      395                      400  
 Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg Phe  
 405                      410                      415  
 Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His Trp  
 420                      425                      430  
 Tyr Ile Thr Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln Ile  
 435                      440                      445  
 Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln Lys  
 450                      455                      460  
 Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn Asp  
 465                      470                      475                      480  
 Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met Leu  
 485                      490                      495  
 Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu Asp  
 500                      505                      510  
 Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu Leu  
 515                      520                      525  
 Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val Asn



530		535		540	
Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser Asn					
545		550		555	560
Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn Asp					
	565		570		575
Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu Asp					
	580		585		590
Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly Ser					
	595		600		605
Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr Ser					
	610		615		620
Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp Leu					
	625		630		635
Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg Pro					
		645		650	655
Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp Lys					
	660		665		670
Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu Lys					
	675		680		685
Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met Lys					
	690		695		700
Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala Ala					
	705		710		715
Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala Leu					
		725		730	735
Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly Met					
	740		745		750
Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn Ser					
	755		760		765
Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val Ala					
	770		775		780
Gly Ser Leu Ser Leu Arg Arg Ala Val Asp Pro Gly Glu Asn Ser Arg					

785 790 795 800

Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser Ser  
805 810 815

Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly Ser  
820 825 830

Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala Leu  
835 840 845

Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala Val  
850 855 860

Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly Gly  
865 870 875 880

His Leu Glu Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu Thr  
885 890 895

Gly Glu Leu Gln Pro Val Leu Pro Glu Gly Ala Ser Ala Ala Pro Glu  
900 905 910

Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys Asp Thr Glu Asn Glu  
915 920 925

Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe Met  
930 935 940

Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Phe Pro Asp  
945 950 955 960

Gly Glu Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu Asn  
965 970 975

Ser Gly Arg

<210> 7

<211> 639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(639)

<400> 7

atg aac cac cag cag cag cag cag cag cag cag aaa gcg ggc gag cag cag	48
Met Asn His Gln Gln Gln Gln Gln Gln Gln Lys Ala Gly Glu Gln Gln	
1 5 10 15	
ttg agc gag ccc gag gac atg gag atg gaa gcg gga gat aca gat gac	96
Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala Gly Asp Thr Asp Asp	
20 25 30	
cca cca aga att act cag aac cct gtg atc aat ggg aat gtg gcc ctg	144
Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn Gly Asn Val Ala Leu	
35 40 45	
agt gat gga cac aac acc gcg gag gag gac atg gag gat gac acc agt	192
Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser	
50 55 60	
tgg cgc tcc gag gca acc ttt cag ttc act gtg gag cgc ttc agc aga	240
Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg	
65 70 75 80	
ctg agt gag tcg gtc ctt agc cct ccg tgt ttt gtg cga aat ctg cca	288
Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro	
85 90 95	
tgg aag att atg gtg atg cca cgc ttt tat cca gac aga cca cac caa	336
Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln	
100 105 110	
aaa agc gta gga ttc ttt ctc cag tgc aat gct gaa tct gat tcc acg	384
Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr	
115 120 125	
tca tgg tct tgc cat gca caa gca gtg ctg aag ata ata aat tac aga	432
Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg	
130 135 140	
gat gat gaa aag tcg ttc agt cgt cgt att agt cat ttg ttc ttc cat	480
Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His	
145 150 155 160	
aaa gaa aat gat tgg gga ttt tcc aat ttt atg gcc tgg agt gaa gtg	528
Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val	
165 170 175	
acc gat cct gag aaa gga ttt ata gat gat gac aaa gtt acc ttt gaa	576
Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu	
180 185 190	

gtc ttt gta cag gcg gat gct ccc cat gga gtt gcg tgg gat tca aag 624  
 Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys  
 195 200 205

aag cac aca ggc tac 639  
 Lys His Thr Gly Tyr  
 210

<210> 8  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Asn His Gln Gln Gln Gln Gln Gln Lys Ala Gly Glu Gln Gln  
 1 5 10 15

Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala Gly Asp Thr Asp Asp  
 20 25 30

Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn Gly Asn Val Ala Leu  
 35 40 45

Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser  
 50 55 60

Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg  
 65 70 75 80

Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro  
 85 90 95

Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln  
 100 105 110

Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr  
 115 120 125

Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg  
 130 135 140

Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His  
 145 150 155 160

Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val  
 165 170 175

Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu  
180 185 190

Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys  
195 200 205

Lys His Thr Gly Tyr  
210

<210> 9

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(540)

<400> 9

atg tca agg gtt cca agt cct cca cct ccg gca gaa atg tcg agt ggc 48  
Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly  
1 5 10 15

ccc gta gct gag agt tgg tgc tac aca cag atc aag gta gtg aaa ttc 96  
Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe  
20 25 30

tcc tac atg tgg acc atc aat aac ttt agc ttt tgc cgg gag gaa atg 144  
Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met  
35 40 45

ggc gaa gtc att aaa agt tct aca ttt tca tca gga gca aat gat aaa 192  
Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys  
50 55 60

ctg aaa tgg tgt ttg cga gta aac ccc aaa ggg tta gat gaa gaa agc 240  
Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser  
65 70 75 80

aaa gat tac ctg tca ctt tac ctg tta ctg gtc agc tgt cca aag agt 288  
Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser  
85 90 95

gaa gtt cgg gca aaa ttc aaa ttc tcc atc ctg aat gcc aag gga gaa 336  
Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu  
100 105 110

gaa acc aaa gct atg gag agt caa cgg gca tat agg ttt gtg caa ggc 384  
 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly  
 115 120 125

aaa gac tgg gga ttc aag aaa ttc atc cgt aga gat ttt ctt ttg gat 432  
 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp  
 130 135 140

gag gcc aac ggg ctt ctc cct gat gac aag ctt acc ctc ttc tgc gag 480  
 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu  
 145 150 155 160

gtg agt gtt gtg caa gat tct gtc aac att tct ggc cag aat acc atg 528  
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met  
 165 170 175

aac atg gta aag 540  
 Asn Met Val Lys  
 180

<210> 10  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly  
 1 5 10 15  
 Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe  
 20 25 30  
 Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met  
 35 40 45  
 Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys  
 50 55 60  
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser  
 65 70 75 80  
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser  
 85 90 95  
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu  
 100 105 110

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly  
 115 120 125

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp  
 130 135 140

Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu  
 145 150 155 160

Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met  
 165 170 175

Asn Met Val Lys  
 180

<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(459)

<400> 11

ttt acc agt gaa tta gtg cca tct tac gat tca gct act ttt gtt tta 48  
 Phe Thr Ser Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu  
 1 5 10 15

gag aat ttc agc act ttg cgt cag aga gca gat cct gtt tac agt cca 96  
 Glu Asn Phe Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro  
 20 25 30

cct ctt caa gtt tca gga ctt tgc tgg agg tta aaa gtt tac cca gat 144  
 Pro Leu Gln Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp  
 35 40 45

gga aat gga gtt gtg cga ggt tac tac tta tct gtg ttt ctg gag ctc 192  
 Gly Asn Gly Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu  
 50 55 60

tca gct ggc ttg cct gaa act tct aaa tat gaa tat cgt gta gag atg 240  
 Ser Ala Gly Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met  
 65 70 75 80

gtt cac cag tcc tgt aat gat cct aca aaa aat atc att cga gaa ttt 288

Val His Gln Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe  
85 90 95

gca tct gac ttt gaa gtt gga gaa tgc tgg ggc tat aat aga ttt ttc 336  
Ala Ser Asp Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe  
100 105 110

cgt ttg gac tta ctc gca aat gaa gga tac ttg aat cca caa aat gat 384  
Arg Leu Asp Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp  
115 120 125

aca gtg att tta agg ttt cag gta cgt tca cca act ttc ttt caa aaa 432  
Thr Val Ile Leu Arg Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys  
130 135 140

tcc cgg gac cag cat tgg tac att act 459  
Ser Arg Asp Gln His Trp Tyr Ile Thr  
145 150

<210> 12

<211> 153

<212> PRT

<213> Homo sapiens

<400> 12

Phe Thr Ser Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu  
1 5 10 15

Glu Asn Phe Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro  
20 25 30

Pro Leu Gln Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp  
35 40 45

Gly Asn Gly Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu  
50 55 60

Ser Ala Gly Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met  
65 70 75 80

Val His Gln Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe  
85 90 95

Ala Ser Asp Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe  
100 105 110

Arg Leu Asp Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp



115

120

125

Thr Val Ile Leu Arg Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys  
 130 135 140

Ser Arg Asp Gln His Trp Tyr Ile Thr  
 145 150

&lt;210&gt; 13

&lt;211&gt; 17

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 13

gcgaattcca ggccgcg

17

&lt;210&gt; 14

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 14

ttcctcgagc cgacttagcc tgtgtgc

27

&lt;210&gt; 15

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 15

cttcgaattc gcgatgtcaa gggttcc

27

&lt;210&gt; 16

&lt;211&gt; 29

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

ccatgctcga ggtattctag ccagaaatg

29

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<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

ccagaattca ccagtgaatt agtgcc

26

---

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

ccactcgagt aatgtaccaa tgctagtcc

29

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<210> 19

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<220>

<221> SITE

<222> (2)..(22)

<223> Xaa = any amino acid

<220>

<221> UNSURE  
<222> (19)..(22)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (24)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (26)..(28)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (30)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (32)..(47)  
<223> Xaa=any amino acid

<220>  
<221> UNSURE  
<222> (47)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (49)..(76)  
<223> Xaa=any amino acid

<220>  
<221> UNSURE  
<222> (73)..(76)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (78)..(93)  
<223> Xaa=any amino acid

<220>  
<221> UNSURE  
<222> (93)  
<223> Xaa may or may not be present

<400> 19

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa

65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp

85 90

<210> 20

<211> 9

<212> PRT

<213> Artificial Sequence

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<222> (2)

<223> Xaa =any amino acid

<220>

<221> SITE

<222> (4)

<223> Xaa=any amino acid

<220>

<221> SITE

<222> (5)

<223> Xaa =Leu or Ile

<220>

<221> SITE

<222> (6)

<223> Xaa =any amino acid

<220>

<221> SITE

<222> (8)  
<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 20

Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro  
1 5

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<210> 21.

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

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<222> (2)..(14)

<223> Xaa=any amino acid

<220>

<221> UNSURE

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<223> Xaa may or may not be present

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<221> SITE

<222> (16)..(22)

<223> Xaa=any amino acid

<220>

<221> SITE

<222> (26)..(28)

<223> Xaa=any amino acid

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<221> SITE

<222> (32)..(42)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (42)

<223> Xaa may or may not be present

<220>

<221> SITE  
 <222> (44)..(47)  
 <223> Xaa = any amino acid

<220>  
 <221> UNSURE  
 <222> (73)..(76)  
 <223> Xaa may or may not be present

<220>  
 <221> SITE  
 <222> (78)..(87)  
 <223> Xaa = any amino acid

<220>  
 <221> UNSURE  
 <222> (87)  
 <223> Xaa may or may not be present

<220>  
 <221> SITE  
 <222> (89)..(93)  
 <223> Xaa=any amino acid

<220>  
 <221> SITE  
 <222> (96)..(98)  
 <223> Xaa=any amino acid

<220>  
 <221> SITE  
 <222> (100)..(115)  
 <223> Xaa=any amino acid

<220>  
 <221> SITE  
 <222> (117)..(123)  
 <223> Xaa=any amino acid

<220>  
 <221> UNSURE  
 <222> (122)..(123)  
 <223> Xaa may or may not be present

<220>  
 <223> Description of Artificial Sequence: Consensus  
 Sequence

<220>  
 <221> UNSURE  
 <222> (22)  
 <223> Xaa may or may not be present

<220>  
 <221> SITE  
 <222> (24)  
 <223> Xaa=any amino acid

<220>  
 <221> SITE  
 <222> (30)  
 <223> Xaa=any amino acid

<220>  
 <221> SITE  
 <222> (49)..(76)  
 <223> Xaa = any amino acid

<400> 21  
 Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa  
 1 5 10 15  
 Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 50 55 60  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Trp Gly Xaa  
 85 90 95  
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 100 105 110  
 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val  
 115 120

<210> 22  
 <211> 124

<212> PRT  
<213> Artificial Sequence

<220>  
<221> SITE  
<222> (2)..(5)  
<223> Xaa =any amino acid

<220>  
<221> SITE  
<222> (6)  
<223> Xaa = Val, Leu, or Ile

<220>  
<221> SITE  
<222> (7)..(14)  
<223> Xaa =any amino acid

<220>  
<221> SITE  
<222> (16)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (17)  
<223> Xaa = Pro or Gly

<220>  
<221> SITE  
<222> (18)..(22)  
<223> Xaa =any amino acid

<220>  
<221> UNSURE  
<222> (22)..(22)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (24)  
<223> Xaa =any amino acid

<220>  
<221> SITE  
<222> (26)  
<223> Xaa =any amino acid



<220>  
<221> SITE  
<222> (27)  
<223> Xaa =Val, Leu or Ile

<220>  
<221> SITE  
<222> (28)  
<223> Xaa = any amino acid

<220>  
<221> SITE  
<222> (30)  
<223> Xaa = any amino acid

<220>  
<221> SITE  
<222> (32)..(42)  
<223> Xaa = any amino acid

<220>  
<221> UNSURE  
<222> (42)..(42)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (44)  
<223> Xaa =Val, Leu or Ile

<220>  
<221> SITE  
<222> (45)..(47)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (49)..(66)  
<223> Xaa=any amino acid

<220>  
<221> UNSURE  
<222> (65)..(66)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
<222> (67)

<223> Xaa=Val, Leu or Ile

<220>

<221> SITE

<222> (68)..(73)

<223> Xaa = any amino acid

<220>

<221> SITE

<222> (74)

<223> Xaa=Asp, Glu, Asn or Gln

<220>

<221> SITE

<222> (75)..(76)

<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<220>

<221> UNSURE

<222> (13)..(14)

<223> Xaa may or may not be present

<220>

<221> UNSURE

<222> (72)..(73)

<223> Xaa may or may not be present

<220>

<221> SITE

<222> (78)..(87)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (87)

<223> Xaa may or may not be present

<220>

<221> SITE

<222> (89)..(93)

<223> Xaa=any amino acid

<220>

<221> SITE

<222> (96)  
<223> Xaa=Trp or Phe

<220>  
<221> SITE  
<222> (97)..(98)  
<223> Xaa=any amino acid

<220>  
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<222> (100)..(104)  
<223> Xaa = any amino acid

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<222> (105)  
<223> Xaa=Val, Leu or Ile

<220>  
<221> SITE  
<222> (106)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (107)  
<223> Xaa=Asp, Glu, Asn or Gln

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<221> SITE  
<222> (108)..(114)  
<223> Xaa=any amino acid

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<223> Xaa=Asp, Glu, Asn or Gln

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<222> (117)  
<223> Xaa=any amino acid

<220>  
<221> SITE  
<222> (118)  
<223> Xaa=Val, Leu or Ile

<220>  
<221> SITE  
<222> (119)..(122)  
<223> Xaa=any amino acid

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~~<221> UNSURE~~  
<222> (121)..(122)  
<223> Xaa may or may not be present

<220>  
<221> SITE  
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<223> Xaa=Asp, Glu, Asn or Gln

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Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa  
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Trp Gly Xaa  
85 90 95

Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
100 105 110

Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val  
115 120

<210> 23  
<211> 139  
<212> PRT  
<213> Homo sapiens

<400> 23  
Asp Met Glu Asp Asp Thr Ser Trp Arg Ser Glu Ala Thr Phe Gln Phe

1	5	10	15
Thr Val Glu Arg Phe Ser Arg Leu Ser Glu Ser Val Leu Ser Pro Pro			
20	25	30	
Cys Phe Val Arg Asn Leu Pro Trp Lys Ile Met Val Met Pro Arg Phe			
35	40	45	
Tyr Pro Asp Arg Pro His Gln Lys Ser Val Gly Phe Phe Leu Gln Cys			
50	55	60	
Asn Ala Glu Ser Asp Ser Thr Ser Trp Ser Cys His Ala Gln Ala Val			
65	70	75	80
Leu Lys Ile Ile Asn Tyr Arg Asp Asp Glu Lys Ser Phe Ser Arg Arg			
85	90	95	
Ile Ser His Leu Phe Phe His Lys Glu Asn Asp Trp Gly Phe Ser Asn			
100	105	110	
Phe Met Ala Trp Ser Glu Val Thr Asp Pro Glu Lys Gly Phe Ile Asp			
115	120	125	
Asp Asp Lys Val Thr Phe Glu Val Phe Val Gln			
130	135		
<210> 24			
<211> 132			
<212> PRT			
<213> Homo sapiens			
<400> 24			
Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met			
1	5	10	15
Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys			
20	25	30	
Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser			
35	40	45	
Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser			
50	55	60	
Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu			
65	70	75	80

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly  
85 90 95

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp  
100 105 110

~~Glu-Ala-Asn-Gly-Leu-Leu-Pro-Asp-Asp-Lys-Leu-Thr-Leu-Phe-Cys-Glu~~  
115 120 125

Val Ser Val Val  
130

<210> 25

<211> 135

<212> PRT

<213> Homo sapiens

<400> 25

Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe  
1 5 10 15

Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln  
20 25 30

Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly  
35 40 45

Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly  
50 55 60

Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln  
65 70 75 80

Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp  
85 90 95

Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp  
100 105 110

Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile  
115 120 125

Leu Arg Phe Gln Val Arg Ser  
130 135

<210> 26

<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 26

Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr Arg Arg Cys His Glu

1 5 10 15

Ser Ala Cys Gly Arg Thr Val Ser Leu Phe Ser Pro Ala Phe Tyr Thr  
20 25 30

Ala Lys Tyr Gly Tyr Lys Leu Cys Leu Arg Leu Tyr Leu Asn Gly Asp  
35 40 45

Gly Thr Gly Lys Arg Thr His Leu Ser Leu Phe Ile Val Ile Met Arg  
50 55 60

Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Arg Asn Lys Val Thr  
65 70 75 80

Phe Met Leu Leu Asp Gln Asn Asn Arg Glu His Ala Ile Asp Ala Phe  
85 90 95

Arg Pro Asp Leu Ser Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr  
100 105 110

Asn Val Ala Ser Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln  
115 120 125

Ser Pro Lys His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys  
130 135 140

Ile Val Glu Thr Ser Thr  
145 150

<210> 27  
<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 27

Gly Val Phe Ile Trp Lys Ile Ser Asp Phe Ala Arg Lys Arg Gln Glu

1 5 10 15

Ala Val Ala Gly Arg Ile Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr  
20 25 30

Ser Arg Tyr Gly Tyr Lys Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp  
35 40 45

Gly Thr Gly Arg Gly Thr His Leu Ser Leu Phe Phe Val Val Met Lys  
50 55 60

Gly Pro Asn Asp Ala Leu Leu Arg Trp Pro Phe Asn Gln Lys Val Thr  
65 70 75 80

Leu Met Leu Leu Asp Gln Asn Asn Arg Glu His Val Ile Asp Ala Phe  
85 90 95

Arg Pro Asp Val Thr Ser Ser Ser Phe Gln Arg Pro Val Asn Asp Met  
100 105 110

Asn Ile Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu  
115 120 125

Ala Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile  
130 135 140

Val Asp Leu Thr Gly Leu  
145 150

<210> 28

<211> 153

<212> PRT

<213> Homo sapiens

<400> 28

Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu  
1 5 10 15

Ala Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr  
20 25 30

Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp  
35 40 45

Gly Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg  
50 55 60

Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr  
65 70 75 80

Leu Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala  
85 90 95



Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Ile Gly Glu  
 100 105 110

Met Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu  
 115 120 125

Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile  
 130 135 140

Val Asp Thr Ser Asp Leu Pro Asp Pro  
 145 150

<210> 29

<211> 163

<212> PRT

<213> Homo sapiens

<400> 29

Gly Val Leu Ile Trp Lys Ile Gly Ser Tyr Gly Arg Arg Leu Gln Glu  
 1 5 10 15

Ala Lys Ala Lys Pro Asn Leu Glu Cys Phe Ser Pro Ala Phe Tyr Thr  
 20 25 30

His Lys Tyr Gly Tyr Lys Leu Gln Val Ser Ala Phe Leu Asn Gly Asn  
 35 40 45

Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg Val Leu Pro  
 50 55 60

Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg Arg Val Thr  
 65 70 75 80

Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys Pro Gln His  
 85 90 95

Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn Phe Gln Lys  
 100 105 110

Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu Gly Phe Gly  
 115 120 125

Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg Asn Tyr Val  
 130 135 140

Arg Asp Asp Ala Val Phe Ile Arg Ala Ala Val Glu Leu Pro Arg Lys

145

150

155

160

Ile Leu Ser

&lt;210&gt; 30

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Gly Lys Leu Ile Trp Lys Val Thr Asp Tyr Lys Met Lys Lys Arg Glu  
 1 5 10 15

Ala Val Asp Gly His Thr Val Ser Ile Phe Ser Gln Ser Phe Tyr Thr  
 20 25 30

Ser Arg Cys Gly Tyr Arg Leu Cys Ala Arg Ala Tyr Leu Asn Gly Asp  
 35 40 45

Gly Ser Gly Arg Gly Ser His Leu Ser Leu Tyr Phe Val Val Met Arg  
 50 55 60

Gly Glu Phe Asp Ser Leu Leu Gln Trp Pro Phe Arg Gln Arg Val Thr  
 65 70 75 80

Leu Met Leu Leu Asp Gln Ser Gly Lys Lys Asn Ile Met Glu Thr Phe  
 85 90 95

Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Arg Pro Asp Gly Glu Met  
 100 105 110

Asn Ile Ala Ser Gly Cys Pro Arg Phe Val Ala His Ser Val Leu Glu  
 115 120 125

Asn Ala Lys Asn Ala Tyr Ile Lys Asp Asp Thr Leu Phe Leu Lys Val  
 130 135 140

Ala Val Asp Leu Thr Asp Leu Glu Asp Leu  
 145 150

&lt;210&gt; 31

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 31

Gly Ile Tyr Ile Trp Lys Ile Gly Asn Phe Gly Met His Leu Lys Cys  
1 5 10 15

Gln Glu Glu Glu Lys Pro Val Val Ile His Ser Pro Gly Phe Tyr Thr  
20 25 30

Gly Lys Pro Gly Tyr Lys Leu Cys Met Arg Leu His Leu Gln Leu Pro  
35 40 45

Thr Ala Gln Arg Cys Ala Asn Tyr Ile Ser Leu Phe Val His Thr Met  
50 55 60

Gln Gly Glu Tyr Asp Ser His Leu Pro Trp Pro Phe Gln Gly Thr Ile  
65 70 75 80

Arg Leu Thr Ile Leu Asp Gln Ser Glu Ala Pro Val Arg Gln Asn His  
85 90 95

Glu Glu Ile Met Asp Ala Lys Pro Glu Leu Leu Ala Phe Gln Arg Pro  
100 105 110

Thr Ile Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val Thr Phe Met His  
115 120 125

Leu Glu Ala Leu Arg Gln Arg Thr Phe Ile Lys Asp Asp Thr Leu Leu  
130 135 140

Val Arg Cys Glu Val Ser Thr Arg Phe Asp Met Gly Ser  
145 150 155

<210> 32

<211> 964

<212> PRT

<213> Homo sapiens

<400> 32

Met Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val Phe Arg Cys Phe  
1 5 10 15

Ile Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser  
20 25 30

Lys Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu Thr Glu Gln Arg  
35 40 45

Ala Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val

50

55

60

Asn Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln  
65 70 75 80

Leu Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu  
85 90 95

Asn His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys  
100 105 110

Ile Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr  
115 120 125

Phe Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn  
130 135 140

Glu Glu Val Ala Lys Leu Arg Arg Arg Leu Met Glu Leu Ile Ser Leu  
145 150 155 160

Val Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg Asn Ala Lys Asp  
165 170 175

Glu Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met Met Ile Ala Arg  
180 185 190

Leu Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys  
195 200 205

Thr Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser Leu Leu Gln Glu  
210 215 220

Val Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys  
225 230 235 240

Ser Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met  
245 250 255

Ala Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu  
260 265 270

Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr  
275 280 285

Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser  
290 295 300

Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val

305                      310                      315                      320  
 Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro  
                                  325                      330                      335  
 Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys  
                                  340                      345                      350  
 Asn Asp Pro Thr Lys Asn Ile Ile Arg Cys Phe Ala Ser Asp Phe Glu  
                                  355                      360                      365  
 Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu  
                                  370                      375                      380  
 Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg  
 385                                   390                      395                      400  
 Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His  
                                  405                      410                      415  
 Trp Tyr Thr Ile Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln  
                                  420                      425                      430  
 Ile Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln  
                                  435                      440                      445  
 Lys Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn  
                                  450                      455                      460  
 Asp Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met  
 465                                   470                      475                      480  
 Leu Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu  
                                  485                      490                      495  
 Asp Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu  
                                  500                      505                      510  
 Leu Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val  
                                  515                      520                      525  
 Asn Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser  
                                  530                      535                      540  
 Asn Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn  
 545                                   550                      555                      560  
 Asp Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu

565

570

575

Asp Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly  
580 585 590

Ser Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr  
595 600 605

Ser Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp  
610 615 620

Leu Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg  
625 630 635 640

Pro Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp  
645 650 655

Lys Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu  
660 665 670

Lys Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met  
675 680 685

Lys Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala  
690 695 700

Ala Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala  
705 710 715 720

Leu Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly  
725 730 735

Met Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn  
740 745 750

Ser Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val  
755 760 765

Ala Gly Ser Leu Ser Leu Arg Arg Ala Val Asp Pro Gly Glu Asn Ser  
770 775 780

Arg Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser  
785 790 795 800

Ser Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly  
805 810 815

Ser Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala

820

825

830

Leu Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala  
835 840 845

Val Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly  
850 855 860

Gly His Leu Phe Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu  
865 870 875 880

Thr Gly Phe Leu Gln Pro Val Leu Pro Glu Gly Ala Ser Ala Ala Pro  
885 890 895

Glu Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Gly Asp Thr Glu Asn  
900 905 910

Glu Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe  
915 920 925

Met Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Glu Pro  
930 935 940

Asp Gly Phe Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu  
945 950 955 960

Asn Ser Gly Arg